

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/562,383
Source: IFWP
Date Processed by STIC: 1/9/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/562,383

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**


- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220>
 

Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 01/09/2006

PATENT APPLICATION: US/10/562,383

TIME: 11:39:50

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Output Set: N:\CRF4\01092006\J562383.raw

3 <110> APPLICANT: Lofton-Day, Cathy; Model, Fabian; Sledziewski, Andrew;
Rujan, Tamas;

4 Lewin, Joern; Distler, Juergen

6 <120> TITLE OF INVENTION: Methods and nucleic acids for the analysis of
colon cell

7 proliferative disorders

W--> 0 <130> FILE REFERENCE:

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/562,383

C--> 10 <141> CURRENT FILING DATE: 2005-12-23

12 <150> PRIOR APPLICATION NUMBER: PCT/US04/20336

13 <151> PRIOR FILING DATE: 2004-06-23

15 <150> PRIOR APPLICATION NUMBER: US 10/679,062

16 <151> PRIOR FILING DATE: 2003-10-03

18 <150> PRIOR APPLICATION NUMBER: US 10/603,138

19 <151> PRIOR FILING DATE: 2003-06-23

21 <150> PRIOR APPLICATION NUMBER: US 10/602,494

22 <151> PRIOR FILING DATE: 2003-06-23

24 <150> PRIOR APPLICATION NUMBER: EP 04090175.3

25 <151> PRIOR FILING DATE: 2004-05-06

27 <150> PRIOR APPLICATION NUMBER: EP 04090072.2

28 <151> PRIOR FILING DATE: 2004-02-27

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ppr 7-9

**Does Not Comply
Corrected Diskette Needed**

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198	<210> SEQ ID NO: 4						
199	<211> LENGTH: 2407						
200	<212> TYPE: DNA						
201	<213> ORGANISM: Homo Sapiens						
203	<400> SEQUENCE: 4						
205	taaggtctgg	gtattctcag	gcagcagggg	caaggtgggc	ttttttcctg	gttgctaaac	60
206	ccacgtcaaa	gtcgagctca	gggactggag	ctcaagaaac	ccaccgccc	ttctccagtc	120
207	cgaccgggga	cctgcatgca	cctctgccgt	gctgccctga	gtcctccaat	cctccacact	180
208	cttctctgt	tatgtacacg	tctccaccca	ggcctgcaaa	agtcccagct	tcctccaggg	240
209	gcagggaccc	gcacgcgggc	ccagggcttg	gcacgcgggg	atgctgaaac	agggccaggc	300
210	ctgggtttcca	gccgatcgtc	agagtcccaa	ggcccagcaa	ccttctctac	aaaggcctcg	360
211	ttaagaggcg	aggaaacaag	agccgggaga	ggggcgcgga	acggcgggcg	ggacgaacga	420
212	ccagctccgc	gcctccggcc	agctcgctcg	agccaggggc	accgcgggct	ttgtgcggct	480

RAW SEQUENCE LISTING

DATE: 01/09/2006

PATENT APPLICATION: US/10/562,383

TIME: 11:39:50

Input Set : N:\DA\PTO.DA.txt

Output Set: N:\CRF4\01092006\J562383.raw

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213 ggaaatctag gaatgggaag gttcggggcc tgctcggctc cggaggcagc tggcgggtcg 540
214 tccctggcgg cgttggagcg gtcagtggca gccgggcacg ggcgaccggg tcgcccgggt 600
215 cgccctcaga ccgtgactcc cgaaaaacct tgcgggcggg gcgcgcccgc gccgtctctt 660
216 gccggaaggt gcgagttagt gcgctcgatt gtgggcgggg gcggaagag gcgcgtttta 720
217 aagtggtaac agatggtttt cttatccaat aggattaaaa aatttgtcct taccggccg 780
218 accgcggaag tagagtaggc gggcggccaa tggggacatg atggggggcg gagccgaggc 840
219 ctccgaagcg gaagtgggtt gctgttgagg cggcggcacg tttctcgagg agctctcctg 900
220 ggcggtgaa gaaggagctt cttctccgga gtgcgcggcg ggtggcgctt gcggacctaa 960
221 ctagctccag gttaggccga gctttgcggg aaagcagcgg taagtcaggg ccttgcagat 1020
222 gcgaggttta ggcagcttcg cggcctacag aggcctcggc ccgcgcctct tgggggagcc 1080
223 gcgctgcgcg gcttgacca gccgaggtt tgcagcccg gacctcgagc cagctctggt 1140
224 cgctgcact gccgtccgcg cgggcgcacc gagcccggt tggcgcgggc aacagaagtt 1200
225 aggaggtctg cgtctgggtc tcggctcacc ctggggggcc gcggccatgg ggcttagttc 1260
226 ctagcctag aagggaact gagactctgg agggggcagg aacgccccca aggtcacttg 1320
227 gaaagtcggg caggatgtgc tgttagggg aagaccggg cagggttttt gttccccgct 1380
228 gacgacgcct cttttgtgtg ttgcgcggc cggcccgcca tcgtggggcc tgcgagtttg 1440
229 ccggggtgcg tgggccgcgt ggcggggcct tttgtaggtc gggaggatct gagtacgggt 1500
230 gcgggcctga ccgtgggggc gccgaggtcg cagtctaaaa cttagtaggg cctcgatttc 1560
231 cgggcgcgct tccgggcccc ggctggtggt tggtggaacg tgcgactgtg aggcttgcg 1620
232 ccagccctg caccgctcgg gcccttcacc gctctggcg gcctatagac aggtgtatga 1680
233 agattctcac gaccgaaac agagttgcta gtaaacaccg cttttccgcc tttgatccat 1740
234 cggggaagag ggaaaaggat agagcttgg caagccgttt tggtagggat ttcagctttt 1800
235 gtctttcact tgtcagttcc catagacgtt caaaaactta ataactctcg ttctgtttct 1860
236 gcaccaagtt cttgagccag acgtagggtc tcagctctgg agcctggctt agactgtcca 1920
237 actgactggg gagactgagg tccagaaaag tgaagtggtc tgcccaaggt cacatagcca 1980
238 gctatttggc agcagatgag gttaagtcc acctgcaaga tttgggtttt gaattcattg 2040
239 accaggagtt ttgggaccac tgtcaataaa agagacattg aagggaatct tttgttactt 2100
240 tcttggatgat ttgcttttta atggacaagg acatattggg ttcagtttta tctgtgagtt 2160
241 tgaggtgaaa tagaggcatt cgagtagcaa gatatttgc tggcttttgt attgcctgaa 2220
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243 cctttgttaag gaccttttgt aaacattggt tttctaactc tcatgaaatc ttaatgccat 2340
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248 <211> LENGTH: 2229
249 <212> TYPE: DNA
250 <213> ORGANISM: Homo Sapiens
252 <400> SEQUENCE: 5
254 tctttcctcg gcgctggctg gtgcgggttg gggtcagggt gagaagccgc tctttgttaa 60
255 ggtgacagaa cgtgctgggg gtggggggccg gggccagggc cggtgcaact agggggccgc 120
256 tgccctttcc tggacacagt ggaagcttct tccgcatcac caaatttttg tcatccttcc 180
257 tgagggacct gcttcaggc agcacgcaag ttgttgtccc gggtttactc cgcacccctc 240
258 tactgggtga ggaaggagca tcttgaatgg agatgggggt gtccccgggt tatacatctg 300
259 cagagaagag gtgtgccggg ctgcacctct ggaggccgcg gtaactgata ttagagaaga 360
260 ccccggttgc agctgggaag gctcactggc tggaaagagg tgccctctcc ttccagcaaa 420
261 gggccctggt tggaaagggt gcttctcacc tgtctagtgg caccacagga cggtcggctt 480
262 ccaactgaat tcccccgac ggtatcatca catagccggg tcctcgaggt gttggtttcc 540
263 caatccgatg actgtcacct cggtaggac ctgtgctgat ggccggagaa ccctgcgctg 600
264 cgggcgcaca tggccagggt gcgcctggca ggcgacgtcc gggtcgagga cggcgctctt 660

```


<210> 674

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 674

gtatgtagtt gtgtggtt

<210> 675

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 675

tttgagtatt cgtaggaa

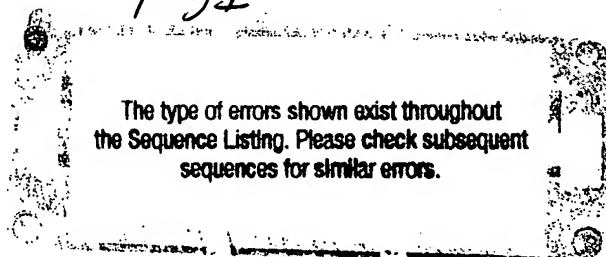
needs explanation on <223> line. Give source of genetic material
(see item 11 on Error summary sheet)

same error

The above sequences
are samples of global
errors

18

FYI



10/562,383 8

<210> 1160
<211> 22
<212> DNA
<213> Artificial Sequence

<220> NEVER has a response, it is a
"header" only. Move this response
to <223> line

<220> bisulfite treated

<223> nucleic acid for analysis of methylation status of SEQ ID NO: 41

<400> 1160

GAGATTGGAG TTTAATTTTG GA

22

change these letters to lower-case. All nucleotide
sequences need to show lower-case letters for
the nucleotides

The above is a sample of global error.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

9

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/562,383

DATE: 01/09/2006
TIME: 11:39:51

FYI

Input Set : N:\DA\PTO.DA.txt
Output Set: N:\CRF4\01092006\J562383.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:51; N Pos. 2126,2128,2131,2132
Seq#:404; N Pos. 2126,2128,2131,2132
Seq#:405; N Pos. 113,114,117,119
Seq#:520; N Pos. 2126,2128,2131,2132
Seq#:521; N Pos. 113,114,117,119

3